Raw Sequence Listing Error Summary

ERROR DETECTED　　**SUGGESTED CORRECTION**　　　**SERIAL NUMBER:** 09/581,651

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
Numbering   use space characters, instead.

4 _____ Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length   Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
"bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence
(OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)　　SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
(NEW RULES)   <210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ✓ Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
"bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

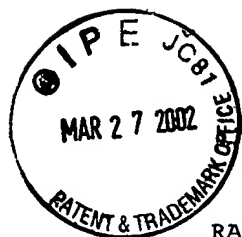**The types of errors shown exist <u>throughout</u> the Sequence Listing. Please check subsequent sequences for similar errors.**

1642

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/581,651

DATE: 08/02/2001
TIME: 17:26:52

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\08022001\I581651.raw

Does Not Comply
Corrected Diskette Needed

Se pag 6 of 7A

```
 4 <110> APPLICANT: Schor, Seth Laurence
 5        Schor, Ana Maria
 7 <120> TITLE OF INVENTION: POLYPEPTIDES, POLYNUCLEOTIDES AND USES
 8        THEREOF
10 <130> FILE REFERENCE: 350013-72
12 <140> CURRENT APPLICATION NUMBER: 09/581,651
13 <141> CURRENT FILING DATE: 2000-10-10
15 <160> NUMBER OF SEQ ID NOS: 15
17 <170> SOFTWARE: FastSEQ for Windows Version 3.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 660
21 <212> TYPE: PRT
22 <213> ORGANISM: Human
24 <400> SEQUENCE: 1
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27    Leu Asn Met Leu Arg Gly Pro Gly Pro Gly Leu Leu Leu Leu Ala Val
28                20                  25                  30
29    Gln Cys Leu Gly Thr Ala Val Pro Ser Thr Gly Ala Ser Lys Ser Lys
30                35                  40                  45
31    Arg Gln Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser
32            50                  55                  60
33    Gln Ser Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn
34    65                  70                  75                  80
35    Gln Gln Trp Glu Arg Thr Tyr Leu Gly Asn Ala Leu Val Cys Thr Cys
36                85                  90                  95
37    Tyr Gly Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu
38                100                 105                 110
39    Glu Thr Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp
40                115                 120                 125
41    Thr Tyr Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile
42            130                 135                 140
43    Gly Ala Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His
44    145                 150                 155                 160
45    Glu Gly Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His
46                165                 170                 175
47    Glu Thr Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys
48                180                 185                 190
49    Gly Glu Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala
50                195                 200                 205
51    Ala Gly Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln
52            210                 215                 220
53    Gly Trp Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg
54    225                 230                 235                 240
55    Ile Thr Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr
56                245                 250                 255
57    Ser Tyr Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn
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58              260                 265                 270
59   Leu Leu Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys
60          275                 280                 285
61   Glu Arg His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe
62       290                 295                 300
63   Thr Asp Val Arg Ala Ala Val Tyr Gln Pro Gln Pro His Pro Gln Pro
64   305                 310                 315                 320
65   Pro Pro Tyr Gly His Cys Val Thr Asp Ser Gly Val Val Tyr Ser Val
66              325                 330                 335
67   Gly Met Gln Trp Leu Lys Thr Gln Gly Asn Lys Gln Met Leu Cys Thr
68              340                 345                 350
69   Cys Leu Gly Asn Gly Val Ser Cys Gln Glu Thr Ala Val Thr Gln Thr
70          355                 360                 365
71   Tyr Gly Gly Asn Ser Asn Gly Glu Pro Cys Val Leu Pro Phe Thr Tyr
72       370                 375                 380
73   Asn Asp Arg Thr Asp Ser Thr Thr Ser Asn Tyr Glu Gln Asp Gln Lys
74   385                 390                 395                 400
75   Tyr Ser Phe Cys Thr Asp His Thr Val Leu Val Gln Thr Arg Gly Gly
76              405                 410                 415
77   Asn Ser Asn Gly Ala Leu Cys His Phe Pro Phe Leu Tyr Asn Asn His
78              420                 425                 430
79   Asn Tyr Thr Asp Cys Thr Ser Glu Gly Arg Arg Asp Asn Met Lys Trp
80          435                 440                 445
81   Cys Gly Thr Thr Gln Asn Tyr Asp Ala Asp Gln Lys Phe Gly Phe Cys
82       450                 455                 460
83   Pro Met Ala Ala His Glu Glu Ile Cys Thr Thr Asn Glu Gly Val Met
84   465                 470                 475                 480
85   Tyr Arg Ile Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly His Met
86              485                 490                 495
87   Met Arg Cys Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile
88          500                 505                 510
89   Ala Tyr Ser Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr
90          515                 520                 525
91   Asn Val Asn Asp Thr Phe His Lys Arg His Glu Glu Gly His Met Leu
92       530                 535                 540
93   Asn Cys Thr Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro
94   545                 550                 555                 560
95   Val Asp Gln Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile Gly
96              565                 570                 575
97   Asp Ser Trp Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys
98          580                 585                 590
99   Tyr Gly Arg Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr Tyr
100             595                 600                 605
101  Pro Ser Ser Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser
102         610                 615                 620
103  Gln Pro Asn Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser His
104  625                 630                 635                 640
105  Ile Ser Lys Tyr Ile Leu Arg Trp Arg Pro Val Ser Ile Pro Pro Arg
106             645                 650                 655
```

```
107  Asn Leu Gly Tyr
108              660
110  <210> SEQ ID NO: 2
111  <211> LENGTH: 2147
112  <212> TYPE: DNA
113  <213> ORGANISM: Human
115  <400> SEQUENCE: 2
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117  ttaggggtcc ggggcccggg ctgctgctgc tggccgtcca gtgcctgggg acagcggtgc     120
118  cctccacggg agcctcgaag agcaagaggc aggctcagca aatggttcag ccccagtccc     180
119  cggtggctgt cagtcaaagc aagcccggtt gttatgacaa tggaaaacac tatcagataa     240
120  atcaacagtg ggagcggacc tacctaggca atgcgttggt ttgtacttgt tatggaggaa     300
121  gccgaggttt taactgcgag agtaaacctg aagctgaaga gacttgcttt gacaagtaca     360
122  ctgggaacac ttaccgagtg ggtgacactt atgagcgtcc taaagactcc atgatctggg     420
123  actgtacctg catcggggct gggcgaggga gaataagctg taccatcgca aaccgctgcc     480
124  atgaaggggg tcagtcctac aagattggtg acacctggag gagaccacat gagactggtg     540
125  gttacatgtt agagtgtgtg tgtcttggta atggaaaagg agaatggacc tgcaagccca     600
126  tagctgagaa gtgttttgat catgctgctg ggacttccta tgtggtcgga gaaacgtggg     660
127  agaagcccta ccaaggctgg atgatggtag attgtacttg cctgggagaa ggcagcggac     720
128  gcatcacttg cacttctaga aatagatgca cgatcagga cacaaggaca tcctatagaa      780
129  ttggagacac ctggagcaag aaggataatc gaggaaacct gctccagtgc atctgcacag     840
130  gcaacggccg aggagagtgg aagtgtgaga ggcacacctc tgtgcagacc acatcgagcg     900
131  gatctggccc cttcaccgat gttcgtgcag ctgtttacca accgcagcct caccccccagc    960
132  ctcctcccta tggccactgt gtcacagaca gtggtgtggt ctactctgtg gggatgcagt    1020
133  ggctgaagac acaaggaaat aagcaaatgc tttgcacgtg cctgggcaac ggagtcagct    1080
134  gccaagagac agctgtaacc cagacttacg gtggcaactc aaatggagag ccatgtgtct    1140
135  taccattcac ctacaacgac aggacggaca gcacaacttc gaattatgag caggaccaga    1200
136  aatactcttt ctgcacagac cacactgttt tggttcagac tcgaggagga aattccaatg    1260
137  gtgccttgtg ccacttcccc ttcctataca acaaccacaa ttacactgat tgcacttctg    1320
138  agggcagaag agacaacatg aagtggtgtg ggaccacaca gaactatgat gccgaccaga    1380
139  agtttgggtt ctgccccatg gctgcccacg aggaaatctg cacaaccaat gaaggggtca    1440
140  tgtaccgcat tggagatcag tgggataagc agcatgacat gggtcacatg atgaggtgca    1500
141  cgtgtgttgg gaatggtcgt ggggaatgga catgcattgc ctactcgcag cttcgagatc    1560
142  agtgcattgt tgatgacatc acttacaatg tgaacgacac attccacaag cgtcatgaag    1620
143  aggggcacat gctgaactgt acatgcttcg gtcagggtcg gggcaggtgg aagtgtgatc    1680
144  ccgtcgacca atgccaggat tcagagactg ggacgtttta tcaaattgga gattcatggg    1740
145  agaagtatgt gcatggtgtc agataccagt gctactgcta tggccgtggc attggggagt    1800
146  ggcattgcca acctttacag acctatccaa gctcaagtgg tcctgtcgaa gtatttatca    1860
147  ctgagactcc gagtcagccc aactcccacc ccatccagtg gaatgcacca cagccatctc    1920
148  acatttccaa gtacattctc aggtggagac ctgtgagtat cccacccaga aaccttggat    1980
149  actgagtctc ctaatcttat caattctgat ggtttctttt tttcccagct tttgagccaa    2040
150  caactctgat taactattcc tatagcattt actatatttg tttagtgaac aaacaatatg    2100
151  tggtcaatta aattgacttg tagactgaaa aaaaaaaaaa aaaaaaa               2147
153  <210> SEQ ID NO: 3
154  <211> LENGTH: 20
155  <212> TYPE: PRT
156  <213> ORGANISM: Human
158  <400> SEQUENCE: 3
159  Ile Ser Lys Tyr Ile Leu Arg Trp Arg Pro Val Ser Ile Pro Pro Arg
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160   1              5                    10                   15
161  Asn Leu Gly Tyr
162              20
164 <210> SEQ ID NO: 4
165 <211> LENGTH: 21
166 <212> TYPE: PRT
167 <213> ORGANISM: Human
169 <400> SEQUENCE: 4
170  Gln Gln Trp Glu Arg Thr Tyr Leu Gly Asn Ala Leu Val Cys Thr Cys
171  1              5                    10                   15
172  Tyr Gly Gly Ser Arg
173              20
175 <210> SEQ ID NO: 5
176 <211> LENGTH: 23
177 <212> TYPE: PRT
178 <213> ORGANISM: Human
180 <400> SEQUENCE: 5
181  Pro Cys Val Leu Pro Phe Thr Tyr Asn Asp Arg Thr Asp Ser Thr Thr
182  1              5                    10                   15
183  Ser Asn Tyr Glu Gln Asp Gln
184              20
186 <210> SEQ ID NO: 6
187 <211> LENGTH: 20
188 <212> TYPE: PRT
189 <213> ORGANISM: Human
191 <400> SEQUENCE: 6
192  Thr Asp His Thr Val Leu Val Gln Thr Arg Gly Gly Asn Ser Asn Gly
193  1              5                    10                   15
194  Ala Leu Cys His
195              20
197 <210> SEQ ID NO: 7
198 <211> LENGTH: 21
199 <212> TYPE: PRT
200 <213> ORGANISM: Human
202 <400> SEQUENCE: 7
203  Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile Ala Tyr Ser Gln Leu
204  1              5                    10                   15
205  Arg Asp Gln Cys Ile
206              20
208 <210> SEQ ID NO: 8
209 <211> LENGTH: 21
210 <212> TYPE: PRT
211 <213> ORGANISM: Human
213 <400> SEQUENCE: 8
214  Gln Gln Trp Glu Arg Thr Tyr Leu Gly Asn Val Leu Val Cys Thr Cys
215  1              5                    10                   15
216  Tyr Gly Gly Ser Arg
217              20
219 <210> SEQ ID NO: 9
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220 <211> LENGTH: 39
221 <212> TYPE: PRT
222 <213> ORGANISM: Human
224 <400> SEQUENCE: 9
225  Glu Pro Cys Val Leu Pro Phe Thr Tyr Asn Gly Arg Thr Phe Tyr Ser
226   1           5               10              15
227  Cys Thr Thr Glu Gly Arg Gln Asp Gly His Leu Trp Cys Ser Thr Thr
228           20              25              30
229  Ser Asn Tyr Glu Gln Asp Gln
230          35
232 <210> SEQ ID NO: 10
233 <211> LENGTH: 21
234 <212> TYPE: PRT
235 <213> ORGANISM: Human
237 <400> SEQUENCE: 10
238  Cys Thr Asp His Thr Val Leu Val Gln Thr Gln Gly Gly Asn Ser Asn
239   1           5               10              15
240  Gly Ala Leu Cys His
241          20
243 <210> SEQ ID NO: 11
244 <211> LENGTH: 21
245 <212> TYPE: PRT
246 <213> ORGANISM: Human
248 <400> SEQUENCE: 11
249  Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Tyr Ala Tyr Ser Gln Leu
250   1           5               10              15
251  Arg Asp Gln Cys Ile
252          20
254 <210> SEQ ID NO: 12
255 <211> LENGTH: 20
256 <212> TYPE: PRT
257 <213> ORGANISM: Human
259 <400> SEQUENCE: 12
260  Ile Ser Lys Tyr Ile Leu Arg Trp Arg Pro Lys Asn Ser Val Gly Arg
261   1           5               10              15
262  Trp Lys Glu Ala
263          20
265 <210> SEQ ID NO: 13
266 <211> LENGTH: 11
267 <212> TYPE: PRT
268 <213> ORGANISM: Human
270 <400> SEQUENCE: 13
271  Thr Ala Ser Gly Val Ala Glu Thr Thr Asn Cys
272   1           5               10
274 <210> SEQ ID NO: 14
275 <211> LENGTH: 24
276 <212> TYPE: PRT
277 <213> ORGANISM: Artificial Sequence
279 <220> FEATURE:
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<210> 14
    <211> 24
    <212> PRT
    <213> Artificial Sequence

    <220>

    <400> 14
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1   5   10   15
Thr Ser Asn Tyr Glu Gln Asp Gln
      20

    <210> 15
    <211> 21
    <212> PRT
    <213> Artificial Sequence

    <220>
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Description of Artificial Sequence is mandatory in Field 223

VERIFICATION SUMMARY DATE: 08/02/2001
PATENT APPLICATION: US/09/581,651 TIME: 17:26:53

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\08022001\I581651.raw

L:281 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: